

Thu May 22 10:43:43 2003

seq1-seql5.res

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq1-seql5.res made by mrulh on Thu 22 May 103 10:27:45-PDT.

Query sequence being compared: US-08-973-363-1 (1-723)
Number of sequences searched: 18
Number of scores above cutoff: 18

Results of the initial comparison of US-08-973-363-1 (1-723) with:
File: US08973363.seq

100-
N -
D 50-
M -
B -
E -
R -
O -
F 10-
S -
S -
Q 5-
Q -
U -
E -
N -
C -
E -
S -
SCORE 0 80 161 241 321 402 482 562 643 723
STDEV 1 1 1 2 3 4 4

PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 500
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
61 19 165.77
Times: CPU
00:00:00.00 Total Elapsed
00:00:00.00

Number of residues: 10306
Number of sequences searched: 18
Number of scores above cutoff: 18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name Description Length Score Score Init. Opt.

1. US-08-973-363-1 Sequence 1, Application US 723 723 723 3.99 0
The list of other best scores is:

Sequence Name Description Length Score Score Init. Opt.

2. US-08-973-363-15 Sequence 15, Application 1316 62 169 0.01 0

1. US-08-973-363-1 (1-723)
US-08-973-363-1 Sequence 1, Application US/08973363

Initial Score = 723 Optimized Score = 723 Significance = 3.99
Residue Identity = 100% Matches = 723 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
CCCGTCGGAGGTTTCAGGAATGACTAGATGGGCACTTAGTCCCATGGTCTAGTGACAAGGTGATGGTT
|||||
X 10 20 30 40 50 60 70
CCCGTCGGAGGTTTCAGGAATGACTAGATGGGCACTTAGTCCCATGGTCTAGTGACAAGGTGATGGTT

80 90 100 110 120 130 140
GGTCAAAAGTTGGACTCGATGATCTCAGAGTCTTCCAGCCCTAATAATCTATGAATCTGTAAATTTA
|||||
80 90 100 110 120 130 140
GGTCAAAAGTTGGACTCGATGATCTCAGAGTCTTCCAGCCCTAATAATCTATGAATCTGTAAATTTA

150 160 170 180 190 200 210
TTCTTGATCTTTTGGAGCAAGTTTGTGGGATTTTGTGTTCCCTGTCACCTGTTCTTCTTCTCTTG
|||||
150 160 170 180 190 200 210
TTCTTGATCTTTTGGAGCAAGTTTGTGGGATTTTGTGTTCCCTGTCACCTGTTCTTCTTCTCTTG

220 230 240 250 260 270 280
AAACTGACTTTTTCAGCAATCAGAAATGCTGTATTGTCAGGTTACAGTACAGTACAGTACAGTACAGT
|||||
220 230 240 250 260 270 280
AAACTGACTTTTTCAGCAATCAGAAATGCTGTATTGTCAGGTTACAGTACAGTACAGTACAGTACAGT

290 300 310 320 330 340 350 360
AGTAGTGAGAAACATTTAGGGAAATACCTGAGTGAGCAACACAGTGGTCTGCTCCCACTGAGCTTTGGG
|||||
290 300 310 320 330 340 350 360
AGTAGTGAGAAACATTTAGGGAAATACCTGAGTGAGCAACACAGTGGTCTGCTCCCACTGAGCTTTGGG

370 380 390 400 410 420 430
ATTGAGAGCCACAGAGTGTATATAATTTGTTAATGATATCTGCTCCCTGCTTCCATTAATGTTG
|||||
370 380 390 400 410 420 430
ATTGAGAGCCACAGAGTGTATATAATTTGTTAATGATATCTGCTCCCTGCTTCCATTAATGTTG

440 450 460 470 480 490 500
TTTTATGAACCACTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT
|||||
440 450 460 470 480 490 500
TTTTATGAACCACTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT

510 520 530 540 550 560 570
ATTGAGAGCCACAGAGTGTATATAATTTGTTAATGATATCTGCTCCCTGCTTCCATTAATGTTG
|||||
510 520 530 540 550 560 570
ATTGAGAGCCACAGAGTGTATATAATTTGTTAATGATATCTGCTCCCTGCTTCCATTAATGTTG

580 590 600 610 620 630 640
AACTATGAGAGTGGAAACAGAAATCTGAGCTAGTTTCTTGGCTGACTGTAAATTTGTTGAGAAATTTTC
|||||
580 590 600 610 620 630 640
AACTATGAGAGTGGAAACAGAAATCTGAGCTAGTTTCTTGGCTGACTGTAAATTTGTTGAGAAATTTTC

650 660 670 680 690 700 710 720
AAGACTACATTAGTTCTGTGTTTGAGGAAAAATAAAATGTTAAGTTGTCCTTCCATTCCTTGAACCTCCGACC

```
|||||
AAGACTACATTAGTTGTTGTTTGGAGAAATAAATGTTTAAAGTTGTCATTCTTCTGAAACCTCCGACC
650 660 670 680 690 700 710 720
|||||
```

```
x
GGG
|||
GGG
x
```

2, US-08-973-363-1 (1-723) 7
US-08-973-363-15, Sequence 15, Application US/08973363 7

Initial Score = 62 Optimized Score = 169 Significance = 0.01
Residue Identity = 32% Matches = 174 Mismatches = 364
Gaps = 3 Conservative Substitutions = 0

```
TCTCTAATTTTATCTTGATCTCTTTTGAGCGAAGTTTGTGTTGGGATTTTGTGTTTCCCTGTCTCACTGT
140 150 160 170 180 x 190 200
|||||
ATTTATCGGCTAGTCACAAAAG
x 10 20
```

```
TTTCTTTTCCCTTGAAACTGACTTTTCATTGTCACATGAGAATGCTGTATTGTCAGGTTACAAGTAGTGCAA
210 220 230 240 250 260 270
|||||
GATCAGTAGAAGAAGATATTCTTGAAGAGCCCAAGAAAAGATGGTGTAGATCATTTAGTTCAGAGAA
30 40 50 60 70 80 90
```

```
280 290 300 310 320 330 340
TGGCTGCTTAGAGTAGTGAGAAACATTTAGGGAAATPACTGGAGTGAAGCAAAACACAGTGGTACTGCCAAAC
|||||
TGGACACACAGAGGAAACTGTACTACATACAGGCTCTACTCTCTTCAAGCTCAACACCTTTTAAATAAGGAAG
100 110 120 130 140 150 160
```

```
350 360 370 380 390 400 410 420
TGTAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCTGCCCTGCTTCC
|||||
AGTTATCAGCAATTTTCAAGTTTGGTCTGAGGAACCTTTTAAAGAACCTGAAANNNGAAGAGAGGAGCCTC
170 180 190 200 210 220 230
```

```
430 440 450 460 470 480 490
ATTAATGCTGTGTTTATGAACACCTCTTTTATTTTGGCTTCTTCATATCCTGCTGCTGTA
|||||
AGGAGATGGATATAGATGAATCTGAGAGGCTGAAACTCGAGAAATGAGTCAGGCCCATTAACCTGTAG
240 250 260 270 280 290 300 310
```

```
500 510 520 530 540 550 560
ATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGGATGACAGTGGTACAGGAGCTCTGA
|||||
GAGATGAGTTTACTTTACAGTTCAAGGTAGCTAACTTTTCCATATGATGAAGATGACATTGAA---TTGG
320 330 340 350 360 370
```

```
570 580 590 600 610 620 630
ATTTTATGATAAATATAGAGTGAAGAACTGAGGCTAGTTCTTCTGAGCTGACTGTAATTTTGT
|||||
AAACAGAAACAAATCTAAGAACTGGGAAAGAAATCATTCAGAAAGTTCAGTGGCGAGCAATAGAGGGGNGG
380 390 400 410 420 430 440 450
```

```
640 650 660 670 680 690 700
GAGAAATTTTCAGACTACATTAGTTGTTGTTGAGGAAATAAATGTTTAAGTTCTCCATTCCTTGA
|||||
AAAGACAAAGAACTTGAAGAAATATATATGCTTCCAGAAATGAGAACTGTGCAAAACAGATCAGCTTTA
460 470 480 490 500 510 520
```

```
710 720 x
AACCTCCCGACCGG
|||||
ATGGAATGAAGGAGGATGCGATGAGGACAGAGATATCTGGATCTGATAGTGAATCCATCTCA
530 540 550 560 570 580
```


2240 2250 2260 2270 2280 2290 2300
2310 2320 2330 2340 2350 2360 2370
GAAGAGTAAAGAGATGAGAAAGTCTTACCTGCTAGGTTGAACAAATCTGAGAGTGAATACAGTG
|||||
GAAGAGTAAAGAGATGAGAAAGTCTTACCTGCTAGGTTGAACAAATCTGAGAGTGAATACAGTG
2310 2320 2330 2340 2350 2360 2370
2380 2390 2400 2410 2420 2430 2440
CATTCAGAGCAATATACAAAGTGGATTTTAAAGCAAGATTTAAAGCCCTCAAGTAAAGTTTCAAAAGGCA
CATTCAGAGCAATATACAAAGTGGATTTTAAAGCAAGATTTTAAAGCCCTCAAGTAAAGTTTCAAAAGGCA
2380 2390 2400 2410 2420 2430 2440
2450 2460 2470 2480 2490 2500 2510 2520
GTACCTCAGGCTTCTGAAACATATGATGAACTTAAAGAGTGTGTAACCATTTGCTCAATTAAGCCAC
|||||
GTACCTCAGGCTTCTGAAACATATGATGAACTTAAAGAGTGTGTAACCATTTGCTCAATTAAGCCAC
2450 2460 2470 2480 2490 2500 2510 2520
2530 2540 2550 2560 2570 2580 2590
CAGATGATATGATTTATATATAACAGAGGCGCTTACAGCATTTGATAGCTAGCAGCGGGAACCTAATCC
|||||
CAGATGATATGATTTATATATAACAGAGGCGCTTACAGCATTTGATAGCTAGCAGCGGGAACCTAATCC
2530 2540 2550 2560 2570 2580 2590
CAGATGATATGATTTATATATAACAGAGGCGCTTACAGCATTTGATAGCTAGCAGCGGGAACCTAATCC
2530 2540 2550 2560 2570 2580 2590
2600 2610 2620 2630 2640 2650 2660
TTCTTGACAGCTTACGATTCGTCGAGAGCGTGGCAACAGAGTTCTGATTTCTCTCAGATGGTGAGA
|||||
TTCTTGACAGCTTACGATTCGTCGAGAGCGTGGCAACAGAGTTCTGATTTCTCTCAGATGGTGAGA
2600 2610 2620 2630 2640 2650 2660
2670 2680 2690 2700 2710 2720 2730
TGCTGGACATCTAGCAGAAATATCTGAAGTATCGCCAGTTTCCCTCCAGAGCTTGATGGATCAATAAAG
|||||
TGCTGGACATCTAGCAGAAATATCTGAAGTATCGCCAGTTTCCCTCCAGAGCTTGATGGATCAATAAAG
2670 2680 2690 2700 2710 2720 2730
2740 2750 2760 2770 2780 2790 2800
GGGAATGAGGAAGCAAGCACTGGATTCATTTCAATGCAAGAGGATCAGAGGATTTCTGTTTACTCTCTA
|||||
GGGAATGAGGAAGCAAGCACTGGATTCATTTCAATGCAAGAGGATCAGAGGATTTCTGTTTACTCTCTA
2740 2750 2760 2770 2780 2790 2800
2810 2820 2830 2840 2850 2860 2870 2880
CAAGAGCTGGAGGATTTAGGTATTAACCTGCGATCTGCGACACTGTAGTATTTCTGCTGAGCTGGAAC
|||||
CAAGAGCTGGAGGATTTAGGTATTTAATCTGCGATCTGCGACACTGTAGTATTTCTGCTGAGCTGGAAC
2810 2820 2830 2840 2850 2860 2870 2880
2890 2900 2910 2920 2930 2940 2950
CACAGATGATCTGAGGACACAGCGAGAGCTCATGAATTTGGACAGAAAGAGGATTTAATTTATCGGC
|||||
CACAGATGATCTGAGGACACAGCGAGAGCTCATGAATTTGGACAGAAAGAGGATTTAATTTATCGGC
2890 2900 2910 2920 2930 2940 2950
2960 2970 2980 2990 3000 3010 3020
TAGTCACAAAGGATCAGTGAAGAAGATATTTCTTGAAGAGCAAGAGAGATGGTGTAGACCATTTAG
|||||
TAGTCACAAAGGATCAGTGAAGAAGATATTTCTTGAAGAGCAAGAGAGATGGTGTAGACCATTTAG
2960 2970 2980 2990 3000 3010 3020
3030 3040 3050 3060 3070 3080 3090
TAATTCAGAGATGAGCAGCAGCAAGAAACTGTTCTCATACAGCTTCAACTCATCAAGCTCTACACCTT
|||||
TAATTCAGAGATGAGCAGCAGCAAGAAACTGTTCTCATACAGCTTCAACTCATCAAGCTCTACACCTT
3030 3040 3050 3060 3070 3080 3090
3100 3110 3120 3130 3140 3150 3160
TTAATAAGAGAGGATTTATCAGCTATTTGAAGTTTGGTGTAGGAACTCTTTAAAGAACTCTGAGGAGAG
|||||
TTAATAAGAGAGGATTTATCAGCTATTTGAAGTTTGGTGTAGGAACTCTTTAAAGAACTCTGAGGAGAG
3100 3110 3120 3130 3140 3150 3160

3170 3180 3190 3200 3210 3220 3230 3240
AACAGGAGCCCAAGGAATGATATAGTGAATCTTGAAGAGAGCTGAATCTCGGAAATGAGCCAGGTC
|||||
AACAGGAGCCCAAGGAATGATATAGTGAATCTTGAAGAGAGCTGAATCTCGGAAATGAGCCAGGTC
3170 3180 3190 3200 3210 3220 3230 3240
3250 3260 3270 3280 3290 3300 3310
CATTCAGCTGTAGGGGATGAGTTGCTTTCACAGTTCAAGTGGGCAACTTTTCCATATGATGAGTGAAGATGATA
|||||
CATTCAGCTGTAGGGGATGAGTTGCTTTCACAGTTCAAGTGGGCAACTTTTCCATATGATGAGTGAAGATGATA
3250 3260 3270 3280 3290 3300 3310
3320 3330 3340 3350 3360 3370 3380
TTGAGTTGGAACCAAGAAATTTCAAGAAATTTGGGAAGAAATCATCCAGAAATCCCAACGGAGAGATAG
|||||
TTGAGTTGGAACCAAGAAATTTCAAGAAATTTGGGAAGAAATCATCCAGAAATCCCAACGGAGAGATAG
3320 3330 3340 3350 3360 3370 3380
3390 3400 3410 3420 3430 3440 3450
AGGAGAGGAAACAGCAAAAAGAACTTGAAGAAATATACATGCTCCGAGGATGAGAACTGTGCAAAAACAGA
|||||
AGGAGAGGAAACAGCAAAAAGAACTTGAAGAAATATACATGCTCCGAGGATGAGAACTGTGCAAAAACAGA
3390 3400 3410 3420 3430 3440 3450
3460 3470 3480 3490 3500 3510 3520
TCAGCTTTATGAGGATGAGGAGAGCGCATGAGGAGAGATATTTCTGATCTGATGAGTGCATCATCA
|||||
TCAGCTTTATGAGGATGAGGAGAGCGCATGAGGAGAGATATTTCTGATCTGATGAGTGCATCATCA
3460 3470 3480 3490 3500 3510 3520
3530 3540 3550 3560 3570 3580 3590 3600
CAGAAAGAAACCGCCCAAAAGAGCGTGGAGACCTCGAAACCATTTCTCGAGAAATATTAAGAGATTAGTG
|||||
CAGAAAGAAACCGCCCAAAAGAGCGTGGAGACCTCGAAACCATTTCTCGAGAAATATTAAGAGATTAGTG
3530 3540 3550 3560 3570 3580 3590 3600
3610 3620 3630 3640 3650 3660 3670
ATGACAGAGATCAGCGGTTTATCAAGAGTTTACAAGAAATTTGGTGGCCCTTGGAAAGTTAGATGCTGTAG
|||||
ATGACAGAGATCAGCGGTTTATCAAGAGTTTACAAGAAATTTGGTGGCCCTTGGAAAGTTAGATGCTGTAG
3610 3620 3630 3640 3650 3660 3670
3680 3690 3700 3710 3720 3730 3740
CTAGAGATGCTGAGTGTGATTAATCTGAGACAGACCTTAGACCTTTGGCTGACCTTACATTAATGGAT
|||||
CTAGAGATGCTGAGTGTGATTAATCTGAGACAGACCTTAGACCTTTGGCTGACCTTACATTAATGGAT
3680 3690 3700 3710 3720 3730 3740
3750 3760 3770 3780 3790 3800 3810
GCATTAAGGCTTTAAAGGACAACTTCTTGGACAAAGAGAGAGGATGATGCTTGGAAAGTTAAAGGCC
|||||
GCATTAAGGCTTTAAAGGACAACTTCTTGGACAAAGAGAGAGGATGATGCTTGGAAAGTTAAAGGCC
3750 3760 3770 3780 3790 3800 3810
3820 3830 3840 3850 3860 3870 3880
CAACCTTTCCAACTCTCAGAGTGGAGGTGAATGCAAAACTAGTCTCTCAGCAAGAGAGGCTGCGACAC
|||||
CAACCTTTCCAACTCTCAGAGTGGAGGTGAATGCAAAACTAGTCTCTCAGCAAGAGAGGCTGCGACAC
3820 3830 3840 3850 3860 3870 3880
3890 3900 3910 3920 3930 3940 3950 3960
TCCCAATCCATCTTCCATCAGATCCAGAGAGGAAAGATATGTCATCCCGACACACAGGCTGCTC
|||||
TCCCAATCCATCTTCCATCAGATCCAGAGAGGAAAGATATGTCATCCCGACACACAGGCTGCTC
3890 3900 3910 3920 3930 3940 3950 3960
3970 3980 3990 4000 4010 4020 4030
ACTTCGATATAGTGGGTAAAGAGATGATTCATCTCTTAGTAGGATCTATGAATATGCTATGGCA
|||||
ACTTCGATATAGTGGGTAAAGAGATGATTCATCTCTTAGTAGGATCTATGAATATGCTATGGCA
3970 3980 3990 4000 4010 4020 4030

4040 4050 4060 4070 4080 4090 4100
GCTGGAAATGATAAAATGGATCCAGATCTCAGCTTAACACAGAAGATTTTACCTGATGATCCAGACAAGA
|||||
GCTGGAAATGATAAAATGGATCCAGATCTCAGCTTAACACAGAAGATTTTACCTGATGATCCAGACAAGA
4040 4050 4060 4070 4080 4090 4100
4110 4120 4130 4140 4150 4160 4170
AATCCCGAGCAAGCAGCTACAGACCCGTCGAGACTACCTCATTAATAATTACTGAATAAAGACCTTGCAGAAA
|||||
AATCCCGAGCAAGCAGCTACAGACCCGTCGAGACTACCTCATTAATAATTACTGAATAAAGACCTTGCAGAAA
4110 4120 4130 4140 4150 4160 4170
4180 4190 4200 4210 4220 4230 4240
AGGAAGACAAAGGCTTCTGGTCAGGCAATCCAGAGAAGGAACACAGAATAAAGAAAGATAAAGATGA
|||||
AGGAAGACAAAGGCTTCTGGTCAGGCAATCCAGAGAAGGAACACAGAATAAAGAAAGATAAAGATGA
4180 4190 4200 4210 4220 4230 4240
4250 4260 4270 4280 4290 4300 4310 4320
AGGCTTCAAAAAATAAAGAAGAAATAAAGAGTGATCTTCACCAACCCCTCAGAAAAATCTGATGAAGATG
|||||
AGGCTTCAAAAAATAAAGAAGAAATAAAGAGTGATCTTCACCAACCCCTCAGAAAAATCTGATGAAGATG
4250 4260 4270 4280 4290 4300 4310 4320
4330 4340 4350 4360 4370 4380 4390
ATGAGGAGGAGGATACCAAGGTAAATGAATCTGAAATTAAGAGAAATCTAAAAAAATTCATTCATTCG
|||||
ATGAGGAGGAGGATACCAAGGTAAATGAATCTGAAATTAAGAGAAATCTAAAAAAATTCATTCATTCG
4330 4340 4350 4360 4370 4380 4390
4400 4410 4420 4430 4440 4450 4460
TGGATATCCAGTTCATATTACTGCAACCGAGTGAACAGTTCCTATCTCAGAAGAAATCTGAAAGACCTCCATC
|||||
TGGATATCCAGTTCATATTACTGCAACCGAGTGAACAGTTCCTATCTCAGAAGAAATCTGAAAGACCTCCATC
4400 4410 4420 4430 4440 4450 4460
4470 4480 4490 4500 4510 4520 4530
AGAAGACATTTAGTGTGCAAGAAAGAAATGAGGCTGTCAAAGCAGCACTGAAACAGCTGGATAGACCCAG
|||||
AGAAGACATTTAGTGTGCAAGAAAGAAATGAGGCTGTCAAAGCAGCACTGAAACAGCTGGATAGACCCAG
4470 4480 4490 4500 4510 4520 4530
4540 4550 4560 4570 4580 4590 4600
AGAAGGGCTTTCTGAAAGGAGCAGCTGGAACATACTAGCAGCTGCTAATCAAAATTTGGGATCATACATTA
|||||
AGAAGGGCTTTCTGAAAGGAGCAGCTGGAACATACTAGCAGCTGCTAATCAAAATTTGGGATCATACATTA
4540 4550 4560 4570 4580 4590 4600
4610 4620 4630 4640 4650 4660 4670 4680
CAGAATGCTGAAGGATGATGATGCTGCAAGAGCTGCAAACTCTACAAACATGCAATCAAAAGCGCCAAAGT
|||||
CAGAATGCTGAAGGATGATGATGCTGCAAGAGCTGCAAACTCTACAAACATGCAATCAAAAGCGCCAAAGT
4610 4620 4630 4640 4650 4660 4670 4680
4690 4700 4710 4720 4730 4740 4750
CCAAAGTTACAGAAATTCATGCCAGAGCTGCAAACTCTACAAACATGCAATCAAAAGCGCCAAAGT
|||||
CCAAAGTTACAGAAATTCATGCCAGAGCTGCAAACTCTACAAACATGCAATCAAAAGCGCCAAAGT
4690 4700 4710 4720 4730 4740 4750
4760 4770 4780 4790 4800 4810 4820
CTCAGCAACAATGACCAAAACATTAGCAGCAATGTGAATACATGTGAATCAGAAATCCAGATGTGGAAA
|||||
CTCAGCAACAATGACCAAAACATTAGCAGCAATGTGAATACATGTGAATCAGAAATCCAGATGTGGAAA
4760 4770 4780 4790 4800 4810 4820
4830 4840 4850 4860 4870 4880 4890
GACTCAAGGAGACTACAAACCATGATAGTACGAGGACAGTATTCTTCGTATAGACATTTATCACAAAT
|||||
GACTCAAGGAGACTACAAACCATGATAGTACGAGGACAGTATTCTTCGTATAGACATTTATCACAAAT
4830 4840 4850 4860 4870 4880 4890
4900 4910 4920 4930 4940 4950 4960

[illegible]


```
|||||
AGCTAGTTGATTAATCTGAACACAGCTTAGACGCTCTGGGAGAGATGTACATAATGGATGCAATTAAAGCGTT
750 760 770 780 790 800 810
3760 3770 3780 3790 3800 3810 3820
TAAAGGACAATTCATCTGGACACAAGACGAGGAGTAGACTTGGGAAAGTTAAAGGCCCAACGTTTCGAA
|||||
TAAATGATAATGACTTTGGTCAAGGAAAGACAGGTGTAGATTGGGAAAGTTAAAGGCCCAACATTCGAA
820 830 840 850 860 870 880
3830 3840 3850 3860 3870 3880 3890 3900
TCTCAGGAGTGCAGGTGAATGCAAAATAGTCTCTCAGGAAGAGAGCTGGCACCACCTGCACAAATTCGA
|||||
TAGCAGAGGTGCAGGTGAATGCAAAATAGTCTCTCAGGAAGAGAGCTGGCACCACCTGCATAAATCGA
890 900 910 920 930 940 950
3910 3920 3930 3940 3950 3960 3970
TTCTCTCAGATCCAGAGAAAGAAAGATATGTCATCCATGCCACCAAGCGTCTCCTCAGTATATAG
|||||
TTCTCTCAGATCCAGAGAAAGAAAGATATGTCATCCATGCCACCAAGCGTCTCCTCAGTATATAG
960 970 980 990 1000 1010 1020 1030
3980 3990 4000 4010 4020 4030 4040
ATTGGGTTAAGAGATGATCCAAATCTGTTAGTGGCATCTATGATATGCTATGGCAGCTGGGAAATGA
|||||
ATTGGGTTAAGAGATGATCCAAATCTGTTAGTGGCATCTATGATATGCTATGGCAGCTGGGAAATGA
1040 1050 1060 1070 1080 1090 1100
4050 4060 4070 4080 4090 4100 4110
TAAATATGATCCAGATCCAGCTTAACACAGAGAGATTTTACCTGATGATCCAGACAAAGACCCCGAGCAA
|||||
TAAATATGATCCAGATCCAGCTTAACACAGAGAGATTTTACCTGATGATCCAGACAAAGACCCCGAGCTA
1110 1120 1130 1140 1150 1160 1170
4120 4130 4140 4150 4160 4170 4180
AGCAGTACAGACCCCTGAGACTACTCTATTAATTAATGATTAAGACCTTGCAGGAAGAGACACAAA
|||||
AGCAGTACAGACTCTGTCAGATCTACTCTATTAATTAATGATTAAGACCTTGCAGGAAGAGACACAGA
1180 1190 1200 1210 1220 1230 1240
4190 4200 4210 4220 4230 4240 4250 X
GGCTCTGCTGTCAGCAATTCACAGAGAGGAGACAGAAATAGAGAAATAA---GATGAAGGCTTCAA
|||||
GACTCTGTCGAGCGCAATTCACAGAGAGGAGAAACAAAGAGTAAAGAGCAATTAAGCAACAAAGGCTGC
1250 1260 1270 1280 1290 1300 1310 X
4260 4270 4280 4290 4300
AATAAAGAGAGAAATAAAGAGTGAATCTTCCACCACACCCCTCAGAA
```

3. US-08-973-363-10 (1-6608)

US-08-973-363-32 Sequence 32, Application US/08973363

Initial Score = 111 Optimized Score = 111 Significance = -0.25
Residue Identity = 100% Matches = 111 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
3450 3460 3470 3480 3490 3500 3510
CAAACAGATCAGCTTTAATGGGAGTGAAGGAGAGCGCAGTAGGACGACAGATATTTCTGGATCTGATAGTG
|||||
ACATATCTCTGGATCTGATAGTG
X
10 20
3520 3530 3540 3550 3560 3570 3580 3590
ACTCCATCACAGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAAATATTAAG
|||||
ACTCCATCACAGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAAATATTAAG
30 40 50 60 70 80 90
3600 X
GATTTAGTGCAGAGATCAGCGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTCGAAAG
|||||
GATTTAGTGCAGAG
```

4. US-08-973-363-10 (1-6608)

US-08-973-363-3 Sequence 3, Application US/08973363

Initial Score = 103 Optimized Score = 115 Significance = -0.25
Residue Identity = 75% Matches = 115 Mismatches = 38
Gaps = 0 Conservative Substitutions = 0

```
4000 4010 4020 4030 4040 4050 4060 4070
TGTTAGTAGCATCTATGAATATGCTATGGCAGCTGGGAAATGATAAAATGGATCCAGATCTCAGCTTAA
|||||
ATTTTACCTGATGATCCAGACA
X
10 20
4080 4090 4100 4110 4120 4130 4140
CACAGAAGATTTTACCTGATGATCCAGACAAGAACCCCGCAAGACGCTACAGACCGCTGACAGACTACC
|||||
AGAAACCCCGCAGGCAAAAGAGCTACAGACCAAGAAACCCCGCAAGACGCTACAGACCGCTGACAGACTACC
30 40 50 60 70 80 90
4150 4160 4170 4180 4190 4200 X 4210
TCATTAATTTACTGAATAAAGACCTTGCAAGAAAGAACGACCAAAAGCGTTGCTGGTGCA
|||||
TCATTAATTTACTGAATAAAGACCTTGCAAGAAAGAACGACCAAAAGCGTTGCTGGTGCA
100 110 120 130 140 150 X
4220 4230 4240 4250
GAAGGAAGACAAGAAATAAGAAGATAAGATGAAGC
```

5. US-08-973-363-10 (1-6608)

US-08-973-363-34 Sequence 34, Application US/08973363

Initial Score = 101 Optimized Score = 101 Significance = -0.26
Residue Identity = 90% Matches = 101 Mismatches = 10
Gaps = 0 Conservative Substitutions = 0

```
3450 3460 3470 3480 3490 3500 3510
CAAACAGATCAGCTTTAATGGGAGTGAAGGAGAGCGCAGTAGGACGACAGATATTTCTGGATCTGATAGTG
|||||
AGATATCTCTGGATCTGATAGTG
X
10 20
3520 3530 3540 3550 3560 3570 3580 3590
ACTCCATCACAGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAAATATTAAG
|||||
ATTCCATCTCAGAAAGAAACGCCCAAAAGCGTGAAGACCTATTTCCCGGTGAAACATTAAG
30 40 50 60 70 80 90
3600 X
GATTTAGTGCAGAGATCAGCGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTGGAAG
|||||
GATTTAGTGCAGAG
100 110
```

6. US-08-973-363-10 (1-6608)

US-08-973-363-36 Sequence 36, Application US/08973363

Initial Score = 99 Optimized Score = 99 Significance = -0.26
Residue Identity = 89% Matches = 99 Mismatches = 12
Gaps = 0 Conservative Substitutions = 0

```
3450 3470 3480 3490 3500 3510 3520
CAGCTTTAATGGGAGTGAAGGAGAGCGCAGTAGGACGACAGATATTTCTGGATCTGATAGTCCATCAC
|||||
GATCTGATAGTACTCCATCTC
X
10 20
3530 3540 3550 3560 3570 3580 3590 3600
AGAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAAATATTAAGGATTTAGTGA
```


[illegible]

3520 3530 3540 3550 3560 3570 3580 3590
 ACTCATTACAGAAAGAAACGGCCAAAAGCGTGGAAAGACCTCGAACCATTCCTCGAAAAATATTAAAG
 ATTCAATCTCGGAAGAAACGGCCGGAAGAAACGTGGCGACCCCGCCATTCCTCGCGGAATATTAAAG
 30 40 50 60 70 80 90

	3600	X	3620	3630	3640	3650
	GATTTAGTGATG	CAGACATG	CAGCGGTTAT	CAAGAGTT	CAAGAAATTT	TGGTGGCCCTCTGGAAG
	GATTTAGTGATG	CGCGAG				
	100	100	110			

12. US-08-973-363-10 (1-6608)
US-08-973-363-33 Sequence 33, Application US/089733363

Initial Score	=	61	Optimized Score	=	61	Significance	=	-0.28
Residue Identity	=	91%	Matches	=	61	Mismatches	=	6
Gaps	=	0	Conservative Substitutions	=	0		=	0

AGTGAAGGACGCCAGTAGGAGCAGAAGATATTCTGGATCTGATAGTGACTTCATCCACAGAAAGAAACGG
3480 3490 3500 3510 3520 3530 3540
||||| ||||| ||||| ||||| |||||
CTCCATCTCGGAAGAGAAACGG
X . 20

3550 3560 3570 3580 3590 3600 3610
 CCANAAAAAGCGTCGAGAGCCCTCGAACCAATTCCTCGAGAAATATTAAAGGATTTTGTAGTCGAGAGATCGAGG
 CCAAAAAAGCGTCGAGAGCCACGCAACTTATTCCTCGAGAAATATA
 30 40 50 60 X

3620 3630
CGGTTTATCAAGAGTTACAAGAA

13. US-08-973-363-10 (1-6608)
US-08-973-363-35 Sequence 35, Application US/08973363

Initial Score	=	59	Optimized Score	=	59	Significance	=	-0.28
Residue Identity	=	88%	Matches	=	59	Mismatches	=	8
Gaps	=	0	Conservative Substitutions	=	0			

AGTGAAGCAAGACGCGTAGTAGGAGCAGGAAGATATTCGTGATCTGATAGTACTCCATCCACAGAAAGAAACCG
3480 3490 3500 3510 3520 3530 3540
CTCCATCTCAGAGAAAGAAAGCA
3550 3560 3570 3580 3590 3600

CCAAAAAGGCTGGAAGACTCGAACATTCTCCAGAAATATTAAAGGATTTAGTGATCGAGAGATCAGG
|||||
CCAGAAAGCTGGAGCCAGCACTATTCCTCGTGAAATATT

3620 3630

14. US-08-973-363-10 (1-6608)
US-08-973-243-1

Initial Score =	49	Optimized Score =	252	Significance =	-0.29
Residue Identity =	38%	Matches =	290	Mismatches =	433

5550	5560	5570	5580	5590	5600	5610
------	------	------	------	------	------	------

GAAAAATATTTTGTATTTAAAGTTTATGCTGCTGCTGCTGCAAAATGTTGTGGCACTTTTTTTTTTAAAGAA
 CCGGTGCGAGGTTTCAAGGAA
 X 10 20

TGCAAGATGTTTACTTTACAGGACCTCAACACTGCCCTTCAGACTGATCTTACTATAAACTCTTCA
TGACTAGATTGGCAGCTTAGTGCCACTGTCTAGTTGCACAAGATGGTGGTCAAAGTTGGACTTCGATGA

5690 5700 5710 5720 5730 5740 5750 5760
TGTCAAAGTGGTCTAGAGCTGAACACAGATTAAATATTTGTAAATGAACATTAACACATGACACCTGTGC
TCTCAGAGTTTTTCCAGCCTTAATA - ATTCTATGAACTCTGTAATTTATCTTCATCTTTTTCAGCGAA

5770 5780 5790 5800 5810 5820 5830
TTATGTTTCAGGAAGAATGGGGAAATTTATTTGTTTATTTCTGTAGAGAACTCTCAAGGACTTTGTTTC
GTTTCTGGGGGAATATGATTGGTCTCCCTGCACTGTTTCTCTTCCCTTGAACATCAC-----TTTTC

5840 5850 5860 5870 5880 5890 5900
 ACTTTCRAAGCTACTTGTTTACATGTCACATGCGACCTTGGCGCTTTTCATCACAAGCTTGTAATATT
 ATTTGCACATGAGATTCCTGCTATTTGTCACGCTTACAACTAGTGCANTAGCTGCTTGAAG-TAGTGAGAA

5910 5930 5940 5950 5960 5970
TAAATCTCTACCTACAGTTGTAAANTAGCCAGATTTCTCTGTTGTGATCAGTTATAATGCGCTTTTAT
ACATTTGAGGAATACATGGAGGTAGCAACA----CAGTGGTACTGCCAACTGTAGCTTTGGGAAITTAG

[illegible]

6050 6060 6070 6080 6090 6100 6110 6120
GTAATTTATTAAATAGCTTTTTTCGCACGCTTTTTTGGCTGTTCCTTCCCAACAACACTCAGCCTT
GCTGTTTATGAACACCACCTTTTTTTTT-----TTTTTTTTTTTTTGCGTCTTCATACTCTGTGGTAAT

6130 6140 6150 6160 6170 6180 6190
CTTTTCACAAAGTCAGTATACATTGTTTTAATAAAATATCCATCGAATCAGAATCTAAAATGGGCA
|||
GAGTTAATGCATTTTAGAACCATCGGCAGCAACTAGSAGATCTGTGGATCACAGTGCTACAGGAGCGCTCTGAAT

AGGGAATATTTTATTCATTGTAGTGCTCTTTTATTGGACTACTTTACACTCTTTTGGTGTGTTTA
TTTTTAGATAAATCATGAGAGTGGAAACAGAAATCTGAGGCTAGTCTTTGAGCTGACTCTAAATTTTGTGA

370 580 590 600 610 620 630
 TTTTATTTTTTTTTTCTATTAAGTCGTCAGTGTGTGTTGTTGTAATGAACAGCTGAGATATCCCACTCTA
 |||||
 GAATATTTTCAAGACTACATAGTTGTGTGCTTTTGAGGAAAAATAAATCTTTTAACTGTGTCATTCCTTTGAAA

	6340	6350	6360	6370	6380	6390	700	711
	AACTGCGCCTGGAAAGCTTTTCAGTCGTCATTCGTTTAAAGAGGAAGTGTCTATAGTGTA							
	CTTCGCGACGGG							

720 X

|||||
AGAAAGAAACGACCAAGAAACGTCAGCAGCAGCAAGCAATATTAAGGATTAGCGCA
30 40 50 60 70 80 90

3610 X 3630 3640 3650 3660
TGCAGAGATCAGCGGTTTATCAGAGAGTTACAGAAATTTGGTGGCCCTCTGGAAGGTTAGATGCT
|||||
TGCAGAGATTAGCGGT
100 110

7. US-08-973-363-10 (1-6608)
US-08-973-363-4 Sequence 4, Application US/08973363

Initial Score = 98 Optimized Score = 111 Significance = -0.26
Residue Identity = 73% Matches = 119 Mismatches = 34
Gaps = 9 Conservative Substitutions = 0

4000 4010 4020 4030 4040 4050 4060
ATTCCAATCTGTTAGTGGCATCTATGAATATGGCTATGGCAGCTGGGAATATGATAAAATGGATCCAGATC
|||||
ATTTTACCTGTATGCCAGATA
X 10 20

4070 4080 4090 4100 4110 4120 4130
TCAGCTTAACAGAGATTTTACCTGTATGATCCAGACAGAAACCCGAGCAAGCAGCTTACAGACCCGTG
|||||
AGAAACCCAGGCTAAGCAGTTA-----CAGACCAAGAAACCCGAGCTAAGCAGTTACAGACCCGTG
30 40 50 60 70 80

4140 4150 4160 4170 4180 4190 4200 X
CAGACTACCTCATTAATAATCTGAATAAGACCTTGAAGAAAGGACACAAAGGCTTGGTGGCAGGCA
|||||
CAGATTACCTCATTAATAATCTGAATAAGACCTTGAAGAAAGGACACAGACTTGGTGGTGA
90 100 110 120 130 140 150 X

4210 4220 4230 4240 4250
ATTCCAAGAGAAGCAAGCAAGAAATAAGAAGATAAGATGAAGGC

8. US-08-973-363-10 (1-6608)
US-08-973-363-5 Sequence 5, Application US/08973363

Initial Score = 94 Optimized Score = 107 Significance = -0.26
Residue Identity = 69% Matches = 107 Mismatches = 46
Gaps = 0 Conservative Substitutions = 0

4000 4010 4020 4030 4040 4050 4060 4070
TGTTAGTAGGCATCTATGAATATGGCTATGGCAGCTGGGAATGATAAAATGGATCCAGATCTCAGCTTAA
|||||
ATTTTACCTGTATGCCAGATA
X 10 20

4080 4090 4100 4110 4120 4130 4140
CACAGAGATTTTACCTGTATGATCCAGACAGAAACCCGAGCAAGCAGCTACAGACCCGTCGAGACTACC
|||||
AGAAACCCAGGCAAGCAGTTCAGACCAAGCAAGAAACCCAGCAAGCAGTTCGAGACCCGTCGAGACTACC
30 40 50 60 70 80 90

4150 4160 4170 4180 4190 4200 X 4210
TCATTAATAATTAATAAGACCTTGAAGAAAGGAGCAAGCAAGGCTTGGTGGCAGGCAATTCGAAGA
|||||
TCATTAATAATTAATAAGACCTTGAAGAAAGGAGCAAGCAAGGCTTGGTGGTGA
100 110 120 130 140 150 X

4220 4230 4240 4250
GAAGGAAGACAAGAAATAAGAAGATAAGATGAAGGC

9. US-08-973-363-10 (1-6608)
US-08-973-363-2 Sequence 2, Application US/08973363

Initial Score = 94 Optimized Score = 96 Significance = -0.26

Residue Identity = 62% Matches = 96 Mismatches = 57
Gaps = 0 Conservative Substitutions = 0

4000 4010 4020 4030 4040 4050 4060 4070
TGTTAGTAGGCATCTATGAATATGGCTATGGCAGCTGGGAATGATAAAATGGATCCAGACTCAGCTTAA
|||||
ATTTTCCAGATGATCCGATA
X 10 20

4080 4090 4100 4110 4120 4130 4140
CACAGAGATTTTACCTGTATGATCCAGACAGAAACCCGAGCAAGCAGCTACAGACCCGTCGAGACTACC
|||||
AAAAACCCAGACCAAGCAAGTTACAGACCAAAACCAAGCAAGCAGTTACAGACCCGTCGAGACTACC
30 40 50 60 70 80 90

4150 4160 4170 4180 4190 4200 X 4210
TCATTAATAATTAATAAGACCTTGAAGAAAGGAGCAAGGCTTGGTGGCAGGCAATTCGAAGA
|||||
TCATCAAACTACTTAGCAGAGATCTTGCAAAAGAGAGGCTCAGAGACTTTGTGTGGC
100 110 120 130 140 150 X

4220 4230 4240 4250
GAAGGAAGACAAGAAATAAGAAGATAAGATGAAGGC

10. US-08-973-363-10 (1-6608)
US-08-973-363-12 Sequence 12, Application US/08973363

Initial Score = 94 Optimized Score = 115 Significance = -0.26
Residue Identity = 45% Matches = 120 Mismatches = 144
Gaps = 1 Conservative Substitutions = 0

4030 4040 4050 4060 4070 4080 4090
ATGCTATGGCAGCTGGGAATGATAAAATGGATCCAGATCTCAGCTTAACAGAGAGATTTTACCTGATG
|||||
GATGAGATTTGTTTCAGTGAAC
X 10 20

4100 4110 4120 4130 4140 4150 4160
ATCCAGACAGAAACCCGAGCAAGCAGCTACAGACCCGTCGAGACTACCTCATTAATTAATTAAG
|||||
ATCTACATAAAATAAAACAGAAAGAAATGAAGAAAGCCTGAGCCAGATTTGGTATATAAGAAAG
30 40 50 60 70 80 90

4170 4180 4190 4200 4210 4220 4230
ACCTTGAAGAAAGGAGCAAGGCTTGGTGGCAGGCAATTCGAAGAGAGAGCAAGAAATAG
|||||
GAAGCTGAAGAAAGGAGAGACAAAGAGAAATAAAAGGGAATTAAGAGGAGGAGAAAGAAAGAA
100 110 120 130 140 150 160

4240 4250 4260 4270 4280 4290 4300
AAGAAATAGATGAAGGCTTCAAAATAAAGCAAGCAATTAAGCTGATCTTCACCAACCCCTCAGAAAA
|||||
GAGATAAGAAAGATTAAGAAAGATTAAGAAAGAGAGAAACAAAGTAAAGATCCACACAG
170 180 190 200 210 220 230

4310 4320 4330 X 4340 4350 4360 4370
TCTCATGATGATGAGGAGGAGGATAACAAGCTAAATGAATGAATCTGAAAAATAAGAAAAATCTAA
|||||
AAGAAAAAGAGTGAAGGAAGAGAG
240 250 260 X

4380
AAAAAT

11. US-08-973-363-10 (1-6608)
US-08-973-363-31 Sequence 31, Application US/08973363

Initial Score = 91 Optimized Score = 94 Significance = -0.26
Residue Identity = 84% Matches = 94 Mismatches = 17
Gaps = 0 Conservative Substitutions = 0


```
TGGAAAGTTAAAGCCCAACATTCCGAATACGAGAGTGCAGGTGAATGCAAAAGCTAGTCAATTTCTCAGCA
860 870 880 890 900 910 920
580
ATAAAATT-----ACAGAAATTCATAGAAATTATTAAAGGCTGGAATAAACTCTGAGATCATCGAGTCCAC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AGAAGAGTTGGCACCATTGGCATAAATCGATTCTCTCAGATCCAGAGAGAAAGAAAGATGTCTATCCCATTA
930 940 950 960 970 980 990 1000
650 660 670 680 690 700 710
TTTGTGACCAACCATCACCTTGTCACTAGACCACTGGCCACTAAGTCCACATCTAGTCTAGTCTCTTGAACCTC
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
CCACACCAAGCAGCTCATTTTGAATAGTTGGGTAAAGAGATGATTCCTCATCTGTAAATAGGCATCTTA
1010 1020 1030 1040 1050 1060 1070
720 X
CGACCGGG
|||
TGAATATGGTTATGGCAGTTGGGAATGATAAAATGGATCCTGTGATCTCAGTTTGACA
1080 1090 1100 1110 1120 1130
```


> O <
O I O Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq10inv-land15.res made by mruhl on Thu 22 May 103 10:40:37-PDT.

Query sequence being compared: US-08-973-363-10' (1-6608)

Number of sequences searched:
Number of scores above cutoff:

Results of the initial comparison of US-08-973-363-10' (1-6608) with:
File : US08973363.seq

100-

N -

U -

M -

B -

E -

R -

O -

F -

S -

E -

Q -

U -

E -

N -

C -

E -

S -

SCORE 0

STDDEV

13

26

0

39

52

64

77

90

103

116

3

2

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 4
Gap penalty 5.00 Window size 30
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 32 Median 24 Standard Deviation 25.32
Times: CPU 00:00:00.03 Total Elapsed 00:00:00.00

Number of residues: 10306
Number of sequences searched: 18
Number of scores above cutoff: 18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Slg. Frame
1. US-08-973-363-10	Sequence 10, Application 6608	116	403	3.32	0
2. US-08-973-363-1	Sequence 1, Application 723	64	257	1.26	0
3. US-08-973-363-13	Sequence 13, Application 137	51	63	0.75	0
4. US-08-973-363-15	Sequence 15, Application 1316	43	432	0.43	0

1. US-08-973-363-10' (1-6608)

US-08-973-363-10 Sequence 10, Application US/08973363

Initial Score = 116 Optimized Score = 403 Significance = 3.32
Residue Identity = 39% Matches = 466 Mismatches = 680
Gaps = 40 Conservative Substitutions = 0

X 10 20
GGTTTTTTGGTTTGTATTA

AAGACTGACATTTTCTGGACCTCTTTTAGCCATATACAGTAACACAGTAATGCGCTTACATCACT
5400 5410 5420 5430 5440 X 5450 5460

TTTAATTTGCAGATAGAAGTTTCTATGACAACTAGTGTGCTTGTACAAATTTCTGTTAATAAGTCACT
116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

CAATCTTCTAAA---ATATTAACTGCTGATAGACACATTTGACATTTATGCCCCATGTTAAAGGGAAC
116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

AAATGATTTACATCAATCTTGGCTGATCTGGGTTTGGAGTGTTCACCTTACAGACACTTCTCTTTTA
170 180 190 200 210 220 230
TTTAAAGAAAGGAA--GATGTTTACTTTTACAGGACCTTACACTGCGCTTTCAGACTGAGCTTACTATA
5610 5620 5630 5640 5650 5660 5670

240 250 260 270 280 290 300
AACCAATCCACCTGAAAGCTTTCCAGG--GCACAGTTTAGTGGGATATCTCCTGTTTCATTCACACAA
116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362

140 150 160 170 180 190 200 210
TTGCCCATGTTAAAGAGGAAACAAATGGATTTACAATGAATCTTGCTGATCTGGGTTTTTGAAGTGTTCAT
150 160 170 180 190 200 210
TTCTTGCATCTTTTGCAGCGAA-----GTTTGTGTTGGGATTTTGTGTTTCCCTGTCACGTGTTTTCTC
220 230 240 250 260 270 280
CCTATAGAACACATCTCTCTCTTTTAAACCAATGCACCTGAAAGCTTTCCAGGCGACAGTTTAGAGTGGGATAT
220 230 240 250 260 270 280
TTCCCTTGAACCTGACTTTCATTTGCAACATGAGAATTGCTGTATTTGTGCAGTTACA-AGTAGTGCAAATGGCGG
290 300 310 320 330 340 350
TGCTTAGAAGTAGTCAGAAACATTTAGGGAATACTCGAGTGAAGCAACACAGTGGTACTGCCAAACCTGAT
360 370 380 390 400 410 420
AAACAGGATGTAAAGATCCCAATAAAAAGGAGCACATAATGAATAAATAAATAAACAACACCAACAA
430 440 450 460 470 480 490
CAATCTGATTCATCGATCGAGATATTTTATTAAACATGTAAAGTAACTACTGCTTTGTGAAAGAAGGCCCTCAGT
500 510 520 530 540 550 560 570
GTTGGGAAAGGAACAGCCAAAAAAGCCTGACGGAAAAAGCTCATTTAAATTAATTTACAATAATTTACAGAG
580 590 600 610 620 630 640
CCATTGTGTGTTTGTGTGTTTTTTTTTTTAAATGTTTTTGTCTGTTTGTGTTTGTTCATAAAGAGGCAT
650 660 670 680 690 700 710
GAATTTTTTAGATAAACAATATGAGATGGAAACAGAAATCTGAGGCTAGTTCTTGAGCTGACTGTAAATTTTT
720 730 740 750 760 770 780
TATAACTGATCAACAACAGGAGAAATCTCGCTATTTTACAACTGTAGGTACAGAAATTAATAATTCACAGCT
790 800 810 820 830 840 850
GTGAGAAATATTTTCAAGACTACATATGTTGTGTGTTTCAGGA----AAAATAAAATTTTTTAAGTTGTCCATTCT
860 870 880 890 900 910
CTTGAACCTCCCGACCGG
920 930 940 950 960 970 980 990
TGTGTAGAAAAGCGCAAGGTGGTCGAGTGTCAAATGTAACAAGTAGCTTTTGGAAAGTGAACAAAGTC
1000 1010 1020 1030 1040 1050 1060 1070
CTTGAACCTCCCGACCGG

3. US-08-973-303-10 (I-0006)
US-08-973-363-13 Sequence 13, Application US/08973363

Initial Score	=	51	Optimized Score	=	63	Significance	=	0.75
Residue Identity	=	48%	Matches	=	69	Mismatches	=	68
Gaps	=		Conservative Substitutions	=			=	0

TCCCTCTCTTTAAACCAATGCACCTGAAAGCTTTCAGGGCACAGTTTAGAGTGGGATATTCTCAGCTCTTCA
 230 240 250 260 270 X 280 290
 TTACAAACATCACACACATGCAGTTTATAGAAAATAAAATAAACCAACCAAAACAGGTATGTAT
 300 310 320 330 340 350 360
 ATCCCATATAAAATAAAGACAG----AAAAGAAATGAAGAAAGATGACCCAGAGATTTGGTATATAA


```

570      580      X      600      610      620      630
TACAGCATTTGTTGGTTTGTGTTGTTTTTTTAAATGTTGTTTGTGTTGTTGTTTCATAAAA
|||||
TAAAGATTTAGTGATGCGAG
90      100      110

```

10. US-08-973-363-10' (1-6608)

US-08-973-363-5 Sequence 5, Application US/08973363

```

Initial Score = 23 Optimized Score = 56 Significance = -0.36
Residue Identity = 39% Matches = 61 Mismatches = 92
Gaps = 1 Conservative Substitutions = 0

```

```

380      390      400      410      420      430      440
GTATCCAATAAAAAAGGAGCAGCACTAAATGGAATAAAATATCCCTCCCACTTTTACATCTGATTCCTCG
|||||
ATTTTACTGATGACCCAGATA
X      10      20

```

```

450      460      470      480      490      500      510
AGATATTTTATTAACATGTAAGTACTGCTTGTGAAAGAGGCGTCAGTTGTTGGGAAGGAACA
|||||
AGAAACACAGGCAAGACAGT-TGCAGACCAAGAACCCAGGCAAGCAGTTGCAGACCCGTGCAGATTAC
30      40      50      60      70      80      90

```

```

520      530      540      550      560      570      580
GCCAAAAAGGCTGAGCGAAAAAGCTCATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
|||||
CTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
100      110      120      130      140      150      160

```

```

590      600      610      620
TTGCTGTTTTTTTTTAAATGTTGTTTGTGTTGTTGTT

```

11. US-08-973-363-10' (1-6608)

US-08-973-363-36 Sequence 36, Application US/08973363

```

Initial Score = 21 Optimized Score = 43 Significance = -0.43
Residue Identity = 38% Matches = 43 Mismatches = 68
Gaps = 0 Conservative Substitutions = 0

```

```

250      260      270      280      290      300      310
GCACCTGAAAAGCTTTCAGGGCACGTTTAGAGTGGGATATCTCACTGTTTCATTAACATACACAC
|||||
GATCTGATAGTGACTCCATCTC
X      10      20

```

```

320      330      340      350      360      370      380
TGACAGTTTATAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
|||||
AGAAAGAAACGACCAAGAACGCTGGACGACCAAGCACTATCCCTCGGGGAGATATATAAGGATTTAGCGA
30      40      50      60      70      80      90

```

```

390      400      410      420      430      440      450
GGAGCAGCTAAATGGAATAAATAATTCCTTCCTCCATTTTACATTTCTGATTCCTCAGATATTTTA
|||||
TGCAGAGATTAGCGGT
100      110

```

12. US-08-973-363-10' (1-6608)

US-08-973-363-33 Sequence 33, Application US/08973363

```

Initial Score = 19 Optimized Score = 31 Significance = -0.51
Residue Identity = 46% Matches = 31 Mismatches = 36
Gaps = 0 Conservative Substitutions = 0

```

```

450      460      470      480      490      500      510
ATATTTTATTAACATGTAAGTATAGTACTGTTGTTGAAAGAGGCGCTGAGTTGTTGGGAAGGAACAGC
|||||

```

```

520      530      540      550      560      570      580
CAAAAAAGGCTGAGCGAAAAAGCTCATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
|||||
CCAAAAAGGCTGGAAGACGACCACTATTAATTCCTCGAGAAAAATA
30      40      50      60      610
GTCGTTTTTTTTTAAATGTTTT

```

13. US-08-973-363-10' (1-6608)

US-08-973-363-34 Sequence 34, Application US/08973363

```

Initial Score = 19 Optimized Score = 44 Significance = -0.51
Residue Identity = 39% Matches = 44 Mismatches = 67
Gaps = 0 Conservative Substitutions = 0

```

```

3670      3680      3690      3700      3710      3720      3730      3740
TAACCTGTTTCTTCTGTCCTCAATCTATGAGCTCTCGCTGTCGAGATCTTCTGCGATTCAGTCAG
|||||
AGATATTCGGATCTGATG
X      10      20

```

```

3750      3760      3770      3780      3790      3800      3810
AATCAAAATAACTACAGTGTGACGAGATGCCAAGTTAATACTTAATCTCCAGCTCTTGTGACAGTAAA
|||||
ATTCCATCTCAGAAAGAAACGACCAAAACGTCGGACGACCACTATTCCTCCGCGTGAACATTAAG
30      40      50      60      70      80      90

```

```

3820      3830      3840      3850      3860      3870
AACAGAAATCTCTGATCCTCTGCAITGAAATGATCCAGTCTTGCTTCTCAATTCCTCTTTAT
|||||
GATTTAGTGATGCAGAG
100      110

```

14. US-08-973-363-10' (1-6608)

US-08-973-363-31 Sequence 31, Application US/08973363

```

Initial Score = 17 Optimized Score = 39 Significance = -0.59
Residue Identity = 35% Matches = 39 Mismatches = 72
Gaps = 0 Conservative Substitutions = 0

```

```

2100      2110      2120      2130      2140      2150      2160      2170
CTTGACAGGCTCATCTTTCTTTGACACACTAAATGCTCTGATGAGTCTTCAGATTCCTCTTGAGA
|||||
AGATATTCGGATCTGATG
X      10      20

```

```

2180      2190      2200      2210      2220      2230      2240
TAGGAACCTGGTTCACTGGTTGCGAGTAATATGAACCTGGAGTATCCAGCAATGGAATTTTTTGTAGATTTCTT
|||||
ATTCAATCTCGAAAGAAACGGCGGAGAAACGTCGGCGACCCGCACTATCCCTCGGAGATATTAAG
30      40      50      60      70      80      90

```

```

2250      2260      2270      2280      2290      2300      2310
TATTTCTGATTTTCATTTTACCTTGTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGA
|||||
GATTTAGTGATGCGGAG
100      110

```

